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- b) isolating a polynucleotide gene expression product from at least one informative gene from one or more cells in said sample; and
 - c) determining a gene expression profile of at least one informative gene, wherein the gene expression profile is correlated with a specific brain tumor sub-type.
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14. (Amended) A method of predicting the efficacy of treating a brain tumor comprising the steps of:

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- a) obtaining a sample of cells derived from a brain tumor;
 - b) isolating a polynucleotide gene expression product from at least one informative gene from one or more cells in said sample; and
 - c) determining a gene expression profile of at least one informative gene, wherein the gene expression profile is correlated with a treatment outcome, thereby classifying the sample with respect to treatment outcome.
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31. (Amended) A method for evaluating drug candidates for their effectiveness in treating brain tumors comprising:

- a) obtaining samples of cells derived from a brain tumor;
- b) isolating a polynucleotide gene expression product from at least one informative gene from one or more cells in said samples; and
- c) determining a gene expression profile of at least one informative gene, wherein the gene expression profile is correlated with the effectiveness of the drug candidate in treating brain tumors.

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32. (Amended) A method for monitoring the efficacy of a brain tumor treatment comprising:

- a) obtaining samples of cells at various time points derived from a patient being treated;
- b) determining the polynucleotide expression profile of the samples;
- c) classifying the samples for treatment outcome based on the expression profile; and

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(157) d) comparing the treatment outcome class of the samples at various times during treatment, wherein the efficacy of brain tumor treatment is determined.

33. (Amended) A method for predicting tumorigenesis comprising:
- a) obtaining samples of cells at various time points derived from a patient;
 - b) determining the polynucleotide expression profile of the samples;
 - c) classifying the samples as tumorigenic or non-tumorigenic based on the expression profile; and
 - d) comparing the tumorigenic class of the samples at various times, such that the onset of tumorigenesis can be predicted.

Please add new Claim 34:

- B4 34. (New) The method of Claim 1, wherein at least one informative gene is FGFR3.

REMARKS

Amendments to Claims

Applicants have cancelled Claims 10, 11, 21 and 22 and amended Claims 1, 14 and 31-33. These amendments have been made consistent with Applicants' election in response to the Restriction Requirement (see below). No new matter has been added. Entry of the amendment is respectfully requested.

Election in Response to Restriction Requirement

Responsive to the Restriction Requirement dated October 15, 2002, the claims of Group I (Claims 1-9, 12-20 and 23-33), drawn to an oligonucleotide microarray, a method of classifying a brain tumor, a method of predicting the efficacy of treating a brain tumor, a method of assigning a brain tumor sample to a treatment class, a method for evaluating drug candidates for their